

Supplementary Table S1. 513 panel gene list

206 full exon coverage and CNV Loss genes									
ABRAXA S1	ACVR1B	ACVR2A	ADAMTS 12	ADAMTS 2	AMER1	APC	ARHGAP 35	ARID1A	ARID1B
ARID2	ARID5B	ASXL1	ASXL2	<b>ATM</b>	<b>ATR</b>	<b>ATRX</b>	AXIN1	AXIN2	B2M
<b>BAP1</b>	<b>BARD1</b>	BCOR	<b>BLM</b>	BMPR2	<b>BRCA1</b>	<b>BRCA2</b>	<b>BRIP1</b>	CASP8	CBFB
CD274	CD276	CDC73	CDH1	CDH10	<b>CDK12</b>	CDKN1A	CDKN1B	CDKN2A	CDKN2B
CDKN2C	<b>CHEK1</b>	<b>CHEK2</b>	CIC	CREBBP	CSMD3	CTCF	CTLA4	CUL3	CUL4A
CUL4B	CYLD	CYP2C9	DAXX	DDX3X	DICER1	DNMT3A	DOCK3	DPYD	DSC1
DSC3	ELF3	ENO1	EP300	EPCAM	EPHA2	ERAP1	ERAP2	ERCC2	ERCC4
ERRF1	ETV6	<b>FANCA</b>	<b>FANCC</b>	<b>FANCD2</b>	<b>FANCE</b>	<b>FANCF</b>	<b>FANCG</b>	<b>FANCI</b>	<b>FANCL</b>
<b>FANCM</b>	FAT1	FBXW7	FUBP1	GATA3	GNA13	GPS2	HDAC2	HDAC9	HLA-A
HLA-B	HNF1A	INPP4B	JAK1	JAK2	JAK3	KDM5C	KDM6A	KEAP1	KMT2A
KMT2B	KMT2C	KMT2D	LARP4B	LATS1	LATS2	MAP2K4	MAP2K7	MAP3K1	MAP3K4
MAPK8	MEN1	MGA	MLH1	MLH3	<b>MRE11</b>	MSH2	MSH3	MSH6	MTAP
MUTYH	<b>NBN</b>	NCOR1	NF1	NF2	NOTCH1	NOTCH2	NOTCH3	NOTCH4	<b>PALB2</b>
PARP1	PARP2	PARP3	PARP4	PBRM1	PDCD1	PDCD1L	PDIA3	PGD	PHF6
PIK3R1	PMS1	PMS2	POLD1	POLE	POT1	PPM1D	<b>PPP2R2A</b>	PRDM1	PRDM9
PRKAR1A	PTCH1	PTEN	PTPRT	<b>RAD50</b>	<b>RAD51</b>	<b>RAD51B</b>	<b>RAD51C</b>	<b>RAD51D</b>	<b>RAD52</b>
<b>RAD54L</b>	RASA1	RASA2	RB1	RBM10	RECQL4	RNASEH2A	RNASEH2B	RNF43	RPA1
RUNX1	SDHA	SDHB	SDHD	SETD2	SLX4	SMAD2	SMAD4	SMARCA4	SMARCB1
SOX9	SPEN	STAG2	STK11	SUFU	TAP1	TAP2	TBX3	TCF7L2	TET2
TGFBR2	TNFAIP3	TNFRSF14	TP53	TP63	TPP2	TSC1	TSC2	USP9X	VHL
WT1	<b>XRCC2</b>	<b>XRCC3</b>	ZFXH3	ZMYM3	ZRSR2				
21 full exon coverage genes									
CALR	CIITA	CYP2D6	ERCC5	FAS	ID3	KLHL13	MTUS2	PSMB10	PSMB8
PSMB9	RNASEH2C	RPL22	RPL5	RUNX1T1	SDHC	SOCS1	STAT1	TMEM132D	UGT1A1
ZBTB20									
108 Hotspot and CNV genes									
ABL1	ABL2	AKT1	AKT2	AKT3	ALK	AR	ARAF	AURKA	AURKC
AXL	BCL2	BCL2L12	BCL6	BRAF	CARD11	CBL	CCND1	CCND2	CCND3
CCNE1	CDK4	CDK6	CHD4	DDR2	EGFR	EIF1AX	ERBB2	ERBB3	ERBB4
ESR1	EZH2	FAM135B	FGFR1	FGFR2	FGFR3	FGFR4	FLT3	FLT4	FOXA1
GATA2	GNAS	H3F3A	H3F3B	IDH2	IKBKB	IL7R	KDR	KIT	KLF5
KRAS	MAGOH	MAP2K1	MAPK1	MAX	MDM4	MECOM	MEF2B	MET	MITF

MPL	MTOR	MYC	MYCN	MYD88	NFE2L2	NRAS	NTRK1	NTRK3	PCBP1
PDGFRA	PDGFRB	PIK3C2B	PIK3CA	PIK3CB	PIK3R2	PIM1	PLCG1	PPP2R1A	PPP6C
PRKACA	PTPN11	PXDNL	RAC1	RAF1	RARA	RET	RHEB	RICTOR	RIT1
ROS1	SETBP1	SF3B1	SLCO1B3	SMC1A	SMO	SPOP	SRC	STAT3	STAT6
TERT	TOP1	TPMT	U2AF1	USP8	XPO1	ZNF217	ZNF429		
<b>61 hotspot genes</b>									
ACVR1	ATP1A1	BCR	BMP5	BTK	CACNA1D	CD79B	CSF1R	CTNNA1	CUL1
CYSLTR2	DGCR8	DROSHA	E2F1	EPAS1	FGF7	FOXL2	FOXO1	GLI1	GNA11
GNAQ	HIF1A	HIST1H2BD	HIST1H3B	HRAS	IDH1	IL6ST	IRF4	IRS4	KLF4
KNSTRN	MAP2K2	MED12	MYOD1	NSD2	NT5C2	NTRK2	NUP93	PAX5	PIK3CD
PIK3CG	PTPRD	RGS7	PIK3CD	PIK3CG	PTPRD	RGS7	RHOA	RPL10	SIX1
SIX2	SNCAIP	SOS1	SOX2	SRSF2	STAT5B	TAF1	TGFB1	TRRAP	TSHR
WAS									
<b>19 CNV Gain genes</b>									
ABCB1	CTNND2	DDR1	EMSY	FGF19	FGF23	FGF3	FGF4	FGF9	FYN
GLI3	IGF1R	MCL1	MDM2	MYCL	RPS6KB1	RPTOR	YAP1	YES1	
<b>86 TMB only genes</b>									
A1CF	ACSM2B	ADAM18	ANO4	ARMC4	BRINP3	C6	C8A	C8B	CANX
CASR	CD163	CNTN6	CNTNAP4	CNTNAP5	COL11A1	DCAF4L2	DCDC1	GALNT17	GPR158
GRID2	HCN1	HLA-C	KCND2	KCNH7	KEL	KIR3DL1	KRTAP2-1	KRTAP6-2	LRRC7
MARCO	NLRC5	NOL4	NRXN1	NYAP2	OR10G8	OR2G6	OR2L13	OR2L2	OR2L8
OR2M3	OR2T3	OR2T33	OR2T4	OR2W3	OR4A15	OR4C15	OR4C6	OR4M1	OR4M2
OR5D18	OR5F1	OR5L1	OR5L2	OR6F1	OR8H2	OR8I2	OR8U1	ORC4	PAK5
PCDH17	PDE1A	PDE1C	PLXDC2	POM121L12	PPFIA2	RBP3	REG1A	REG1B	REG3A
REG3G	RPTN	RUNDC3B	SH3RF2	SLC15A2	SLC8A1	SYT10	SYT16	TAPBP	TPTE
TRHDE	TRIM48	TRIM51	ZIM3	ZNF479	ZNF536				
<b>51 Fusion drivers genes</b>									
AKT2	ALK	AR	AXL	BRAF	BRCA1	BRCA2	CDKN2A	EGFR	ERBB2
ERBB4	ERG	ESR1	ETV1	ETV4	ETV5	FGFR1	FGFR2	FGFR3	FGR
FLT3	JAK2	KRAS	MDM4	MET	MYB	MYBL1	NF1	NOTCH1	NOTCH4
NRG1	NTRK1	NTRK2	NTRK3	NUTM1	PDGFR A	PDGFRB	PIK3CA	PPARG	PRKACA
PRKACB	PTEN	RAD51B	RAF1	RB1	RELA	RET	ROS1	RSPO2	RSPO3
TERT									

\*\*Genes of the homologous recombination (HR) complex are in blue color

Supplementary Table S2. 513 panel gene list

87 hotspot genes									
AKT1	AKT2	AKT3	ALK	AR	ARAF	AXL	BRAF	BTK	CBL
CCND1	CDK4	CDK6	<b>CHEK2</b>	CSF1R	CTNNB1	DDR2	EGFR	ERBB2	ERBB3
ERBB4	ERCC2	ESR1	EZH2	FGFR1	FGFR2	FGFR3	FGFR4	FLT3	FOXL2
GATA2	GNA11	GNAQ	GNAS	H3F3A	HIST1H3B	HNF1A	HRAS	IDH1	IDH2
JAK1	JAK2	JAK3	KDR	KIT	KNSTRN	KRAS	MAGOH	MAP2K1	MAP2K2
MAP2K4	MAPK1	MAX	MDM4	MED12	MET	MTOR	MYC	MYCN	MYD88
NFE2L2	NRAS	NTRK1	NTRK2	NTRK3	PDGFRA	PDGFRB	PIK3CA	PIK3CB	PPP2R1A
PTPN11	RAC1	RAF1	RET	RHEB	RHOA	ROS1	SF3B1	SMAD4	SMO
SPOP	SRC	STAT3	TERT	TOP1	U2AF1	XPO1			
48 full exon coverage									
ARID1A	<b>ATM</b>	<b>ATR</b>	<b>ATR</b>	<b>ATR</b>	<b>BAP1</b>	<b>BRCA1</b>	<b>BRCA2</b>	CDK12	CDKN2A
CDKN2B	<b>CHEK1</b>	CREBBP	<b>FANCA</b>	<b>FANCD2</b>	<b>FANCI</b>	FBXW7	MLH1	<b>MRE11</b>	MSH2
MSH6	<b>NBN</b>	NF1	NF2	NOTCH1	NOTCH2	NOTCH3	<b>PALB2</b>	PIK3R1	PMS2
POLE	PTCH1	PTEN	<b>RAD50</b>	<b>RAD51</b>	<b>RAD51C</b>	<b>RAD51D</b>	<b>RAD51B</b>	RB1	RNF43
SETD2	SLX4	SMARCA4	SMARCB1	STK11	TP53	TSC1	TSC2		
43 copy number variants									
AKT1	AKT2	AKT3	ALK	AR	AXL	BRAF	CCND1	CCND2	CCND3
CCNE1	CDK2	CDK4	CDK6	EGFR	ERBB2	ESR1	FGF19	FGF3	FGFR1
FGFR2	FGFR3	FGFR4	FLT3	IGF1R	KIT	KRAS	MDM2	MDM4	MET
MYC	MYCL	MYCN	NTRK1	NTRK2	NTRK3	PDGFRA	PDGFRB	PIK3CA	PIK3CB
PPARG	RICTOR	TERT							
51 fusion drivers									
AKT2	ALK	AR	AXL	BRAF	<b>BRCA1</b>	<b>BRCA2</b>	CDKN2A	EGFR	ERBB2
ERBB4	ERG	ESR1	ETV1	ETV4	ETV5	FGFR1	FGFR2	FGFR3	FGR
FLT3	JAK2	KRAS	MDM4	MET	MYB	MYBL1	NF1	NOTCH1	NOTCH4
NRG1	NTRK1	NTRK2	NTRK3	NUTM1	PDGFRA	PDGFRB	PIK3CA	PPARG	PRKACA
PRKACB	PTEN	<b>RAD51B</b>	RAF1	RB1	RELA	RET	ROS1	RSPO2	RSPO3
TERT									

\*\*Genes of the homologous recombination (HR) complex are in blue color

Supplementary Table S3. Study population and biomarkers' results obtained

Patient	Age	Gender	NGS results	PD-L1	TMB	MSI
<u>1</u>	39	Female	KRAS:c.35G>A (p.G12D)			
<u>2</u>	68	Female				

<u>3</u>	57	Male	KRAS:c.35G>A (p.G12D) ERBB2:c.1998_1999 delCT (p.L667fs*36) CDKN2A:c.83_100delTGCGGGCGCTGCTGGAG G (-) TP53:c.818G>A (p.R273H)			
<u>4</u>	60	Female	TP53:c.380C>A (p.Ser127Tyr)			
<u>5</u>	61	Male				
<u>6</u>	64	Male				
<u>7</u>	36	Female	KRAS:c.35G>A (p.G12D) TP53:c.796G>A (p.G266R) CCNE1:Amplification			
<u>8</u>	61	Male	FGFR4:Amplification			
<u>9</u>	60	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.817C>T (p.Arg273Cys)			
<u>10</u>	71	Male	TP53:c.607G>A (p.Val203Met)			
<u>11</u>	38	Male	TP53:c.557A>G (p.D186G)			
<u>12</u>	48	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.215_216 insG (p.Val73fs)			
<u>13</u>	63	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.430C>T (p.Gln144Ter)			
<u>14</u>	64	Female	KRAS:c.35G>A (p.Gly12Asp)			
<u>15</u>	54	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.532C>T (p.His178Tyr) ATM:c.9022C>T (p.Arg3008Cys) TSC1:c.433C>T (p.Gln145Ter) CREBBP:c.6019 C>T (p.Gln2007Ter)			

<u>16</u>	69	Male	KRAS:c.35G>T (p.Gly12Val)			
<u>17</u>	48	Male	KRAS:c.35G>T (p.Gly12Val)			
<u>18</u>	51	Male	TSC2:c.2380C>T (p.Q794*) STK11:c.465- 1G>A STK11:c.465-1G>A		32,24	
<u>19</u>	65	Female	KRAS:c.35G>A (p.Gly12Asp) RNF43:c.2057_2 058insG (p.Ser687fs) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative <1%	negative  <1%	7,93	STABLE (MSS)
<u>20</u>	67	Male	KRAS:c.35G>T (p.Gly12Val)		fail	
<u>21</u>	59	Female	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative insufficient material	negative  i nsufficient material	12,2	STABLE (MSS)
<u>22</u>	47	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.706T>A (p.Tyr236Asn)		11,81	
<u>23</u>	45	Female	KRAS:c.35G>T (p.Gly12Val)		45,21	
<u>24</u>	81	Female	TP53:c.743G>A (p.Arg248Gln) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative <1%	negative  <1%	13,17	STABLE (MSS)
<u>25</u>	63	Male	KRAS:c.35G>A (p.Gly12Asp)		18,11	
<u>26</u>	62	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.823delT (p.Cys275fs)		14,1	

<u>27</u>	73	Male	KRAS:c.34_35delGGinsCT (p.G12L) CDK12:c.3283delG (p.E1095fs) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:fail fail	fail fail	21,67	STABLE (MSS)
<u>28</u>	55	Male	TP53:c.517G>A (p.Val173Met) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:fail fail	fail fail	18,08	STABLE (MSS)
<u>29</u>	67	Male	KRAS:c.37G>T (p.Gly13Cys)		19,03	
<u>30</u>	63	Male	KRAS:c.183A>C (p.Gln61His) TP53:c.646G>A (p.Val216Met) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative <1%	negative  <1%	18,97	STABLE (MSS)
<u>31</u>	71	Female	KRAS:c.35G>T (p.Gly12Val) SMARCA4:c.293 5C>T (p.Arg979Ter)		13,1	
<u>32</u>	78	Male	KRAS:c.35G>A (p.Gly12Asp) PIK3R1:c.211G> T (p.Gly71Ter)		22,27	
<u>33</u>	53	Female	Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative insufficient material	negative  i nsufficient material	20,99	STABLE (MSS)
<u>34</u>	58	Male	TP53:c.532C>T (p.His178Tyr)		1,16	

<u>35</u>	68	Male	KRAS:c.35G>A (p.Gly12Asp) CDKN2A:c.221deA (p.Leu74fs) TP53:c.659A>G (p.Tyr220Cys) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive 25%	positive 2 5%	25,01	STABLE (MSS)
<u>36</u>	44	Female	KRAS:c.35G>T (p.Gly12Val) CDKN2A:c.233_2 34delTC (p.Leu78fs) RNF43:c.2057_20 58insG (p.Ser687fs)		32,1	
<u>37</u>	50	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.527G>T (p.Cys176Phe)		23,76	
<u>38</u>	77	Female	KRAS:c.35G>T (p.Gly12Val) POLE:c.6649C>T (p.Gln2217Ter)		23,69	
<u>39</u>	68	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.646G>A (p.Val216Met)		2,72	
<u>40</u>	28	Female	PIK3CA:c.3140A>G (p.H1047R) MSH2:Loss (Oncogenic Mutations) Microsatellite Instability (MSI):HIGH (MSI- High) PD-L1 expression:positive 60%	positive 6 0%	13,45	HIGH (MSI- High)
<u>41</u>	47	Male	TP53:c.211_220delCCCCCGT GG (p.Pro72fs)		2,8	
<u>42</u>	68	Male	Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative <1%	negative  <1%	12,4	STABLE (MSS)
<u>43</u>	80	Female	KRAS:c.35G>T (p.Gly12Val)		3,6	

<u>44</u>	68	Male	PALB2:c.1037_1041delAAGAA (p.Lys346Thrfs)		8,03	
<u>45</u>	48	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:positive 2%	positive  2 %	6,8	STABLE (MSS)
<u>46</u>	80	Male	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.818G>A (p.Arg273His)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:negative <1%	negative  <1%	0,94	STABLE (MSS)
<u>47</u>	75	Male	KRAS:c.35G>A (p.Gly12Asp)		4,44	
<u>48</u>	57	Male			1,68	
<u>49</u>	54	Female	KRAS:c.34G>C (p.Gly12Arg)		4,52	
<u>50</u>	51	Female	KRAS:c.35G>T (p.Gly12Val)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:negative <1%	negative  <1%	fail	STABLE (MSS)
<u>51</u>	44	Male	KRAS:c.34G>C (p.Gly12Arg)  TP53:c.916C>T (p.Arg306Ter)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:fail fail	fail  fail	9,05	STABLE (MSS)
<u>52</u>	67	Male	KRAS:c.34G>C (p.Gly12Arg)		5,18	

<u>53</u>	43	Male	KRAS:c.38G>A (p.Gly13Asp)  TP53:c.524G>A (p.Arg175His)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:negative <1%	negative  <1%	12,74	STABLE (MSS)
<u>54</u>	52	Male	KRAS:c.34G>C (p.Gly12Arg)		6	
<u>55</u>	58	Female	FGFR1 fusion:WHSC1L1(1)-FGFR1(2)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:negative <1%	negative  <1%	3,4	STABLE (MSS)
<u>56</u>	53	Female	KRAS:c.35G>T (p.Gly12Val)  SLX4:c.212C>G (p.Ser71Ter)  TP53:c.743G>A (p.Arg248Gln)  PPARG fusion:TSEN2(5)-PPARG(4)		1,52	
<u>57</u>	61	Female	KRAS:c.35G>A (p.Gly12Asp)		2,97	
<u>58</u>	59	Male	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.725G>T (p.Cys242Phe)  RSPO2 fusion:EIF3E(1)-RSPO2(2)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:positive 30%	positive  30%	5,44	STABLE (MSS)
<u>59</u>	66	Female	KRAS:c.35G>A (p.Gly12Asp)  CDKN2A:c.172C>T (p.Arg58Ter)  TP53:c.818G>A (p.Arg273His)		4,2	

<u>60</u>	51	Male	FANCA:c.3094C>T (p.Gln1032Ter)  KRAS:c.35G>A (p.Gly12Asp)  STK11:c.923G>A (p.Trp308Ter)  STK11:c.923G>A (p.Trp308Ter)  TP53:c.310C>T (p.Gln104Ter)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:negative <1%	negative  <1%	fail	STABLE (MSS)
<u>61</u>	73	Female	KRAS:c.35G>T (p.Gly12Val)  PIK3CA:c.3139C>T (p.His1047Tyr)		20	
<u>62</u>	39	Male	PALB2:c.1140_1143delTCTT (p.Ser380fs)		0,9	
<u>63</u>	49	Male	TP53:c.916C>T (p.Arg306Ter)		9,4	
<u>64</u>	64	Female	KRAS:c.35G>T (p.Gly12Val)		29,6	
<u>65</u>	65	Female	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.731G>T (p.Gly244Val)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:positive TC 15%, IC 1%	positive  TC 15%, IC 1%	4,33	STABLE (MSS)
<u>66</u>	58	Male	KRAS:c.35G>T (p.Gly12Val)  CDKN2A:c.7G>T (p.Glu27Ter)  TP53:c.646G (p.Val216Leu)  Microsatellite Instability (MSI):STABLE (MSS)  PD-L1 expression:positive TC<1%, IC<1%	positive  TC<1%, IC<1%	10,81	STABLE (MSS)
<u>67</u>	73	Male			4,05	

<u>68</u>	59	Female	KRAS:c.35G>A (p.Gly12Asp) SMAD4:c.1576G >T (p.Glu526Ter) TP53:c.733G>A (p.Gly245Ser)		18,59	
<u>69</u>	71	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC<1%, IC 5%	positive T C<1%, IC 5%	4,02	STABLE (MSS)
<u>70</u>	61	Male	MLH1:c.1292_1293insC (p.Met431fs) FBXW7:c.1629_ 1630delAG (p.Arg543fs) FBXW7:c.1099C> T (p.Arg367Ter) CDKN2B:c.244 C>T (p.Arg82Ter)			
<u>71</u>	71	Male	KRAS:c.34G>C (p.Gly12Arg)		6,13	
<u>72</u>	54	Male	KRAS:c.38G>A (p.Gly13Asp) TP53:c.742C>T (p.Arg248Trp) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC>10%, IC>50%	positive T C>10%, IC>50%	3,65	STABLE (MSS)
<u>73</u>	41	Male	KRAS:c.35G>A (p.Gly12Asp)			
<u>74</u>	61	Female	KRAS:c.34G>C (p.Gly12Arg)			
<u>75</u>	80	Male	KRAS:c.35G>A (p.Gly12Asp)			
<u>76</u>	57	Male	KRAS:c.183A>C (p.Gln61His)			

<u>77</u>	73	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.577C>T (p.His193Tyr) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC <1%, IC 1%	positive T C <1%, IC 1%	8,32	STABLE (MSS)
<u>78</u>	70	Male	KRAS:c.35G>T (p.Gly12Val) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative IC<1%	negative I C<1%	27,31	STABLE (MSS)
<u>79</u>	84	Female	NF2:c.1331C>A (p.Ser444Ter) NF2:c.1294G>T (p.Glu432Ter) TP53:c.817C>T (p.Arg273Cys) MYC:Amplifica tion		25,45	
<u>80</u>	69	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.480_496 delGGCTCTAAGGT (p.Met160fs) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC 10%, IC<1%	positive T C 10%, IC<1%	5,18	STABLE (MSS)
<u>81</u>	58	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.839G>C (p.Arg280Thr)		12,85	
<u>82</u>	57	Male	Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative ncelled	negative  ncelled	2,57	STABLE (MSS)
<u>83</u>	57	Female				
<u>84</u>	61	Male	KRAS:c.34G>T (p.Gly12Cys) TP53:c.524G>A (p.Arg175His)			

<u>85</u>	55	Male	KRAS:c.35G>A (p.Gly12Asp) PIK3CA:c.1633G>A (p.Glu545Lys) TP53:c.524G>A (p.Arg175His)			
<u>86</u>	56	Male	KRAS:c.35G>A (p.Gly12Asp) MET fusion:MET(13)- MET(15) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC<1%, IC<1%	negative  TC<1%, IC<1%	fail	STABLE (MSS)
<u>87</u>	67	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative TC<1%, IC<1%	negative  TC<1%, IC<1%	9,35	STABLE (MSS)
<u>88</u>	55	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC 1%, IC<1%	positive T C 1%, IC<1%	2,54	STABLE (MSS)
<u>89</u>	64	Female	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC<1%, IC 20%	positive T C<1%, IC 20%	1,72	STABLE (MSS)
<u>90</u>	63	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.566_567i nsCCCT (p.Gln192fs)			
<u>91</u>	64	Female	KRAS:c.35G>A (p.Gly12Asp) PIK3CA:c.331A> G (p.Lys111Glu) CDKN2A:c.172 C>T (p.Arg58Ter) TP53:c.472C>G (p.Arg158Gly)		3,97	

<u>92</u>	71	Female	KRAS:c.34G>C (p.Gly12Arg) CDKN2A:c.47_50delTGGC (p.Leu16fs) TP53:c.743G>A (p.Arg248Gln) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC<1%, IC 20%	positive TC<1%, IC 20%	11,14	STABLE (MSS)
<u>93</u>	73	Female	KRAS:c.35G>T (p.Gly12Val)			
<u>94</u>	56	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.578A>G (p.His193Arg) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC<1%, IC 25%	positive TC<1%, IC 25%	2,57	STABLE (MSS)
<u>95</u>	44	Female	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC1%, IC<1%	positive TC1%, IC<1%	8,03	STABLE (MSS)
<u>96</u>	45	Male	Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:negative TC<1%, IC<1%	negative TC<1%, IC<1%	18,38	STABLE (MSS)
<u>97</u>	73	Male	KRAS:c.35G>T (p.Gly12Val)			
<u>98</u>	68	Male	KRAS:c.183A>C (p.Gln61His) TP53:c.524G>A (p.Arg175His) ERBB2:Amplification			
<u>99</u>	61	Male			14,63	
<u>100</u>	72	Male	KRAS:c.35G>T (p.Gly12Val) CDKN2A:c.135_138delTCGG (p.Arg46fs)			
<u>101</u>	72	Female	KRAS:c.34G>C (p.Gly12Arg)			

<u>102</u>	65	Male	KRAS:c.35G>A (p.Gly12Asp) ARID1A:c.646deA (p.Ser2156fs) TP53:c.742C>T (p.Arg248Trp)			
<u>103</u>	51	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.526T>A (- ) : :			
<u>104</u>	57	Female	KRAS:c.35G>A (p.Gly12Asp) CDKN2A:c.247C >T (p.His83Tyr) TP53:c.226_227i nsG (p.Ala76fs) Microsatellite Instability (MSI):STABLE (MSS) PD-L1 expression:positive TC 10%, IC 1%	positive T C 10%, IC 1%	6,12	STABLE (MSS)
<u>105</u>	53	Female	NBN:c.657_661delACAAA (p.Lys219Asnfs*16)			
<u>106</u>	56	Female	KRAS:c.35G>T (p.Gly12Val) STK11:c.464+1G >A STK11:c.464+1G>A			
<u>107</u>	80	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.586C>T (p.Arg196Ter) TP53:c.173delC (p.Pro58fs)			
<u>108</u>	64	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.577C>T (p.His193Tyr)			
<u>109</u>	67	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.832C>T (p.Pro278Ser)			
<u>110</u>	54	Male	KRAS:c.34G>C (p.Gly12Arg) KRAS:amplificati on MYC:amplification CCND3 :amplification			
<u>111</u>	60	Male	KRAS:c.35G>A (p.Gly12Asp) TP53: c.833C>T (p.Pro278Leu)			
<u>112</u>	66	MAle	KRAS:c.35G>A (p.Gly12Asp) GNAS:c.602G>A (p.Arg201His)			

<u>113</u>	64	Male				
<u>114</u>	62	Female	KRAS:c.35G>T (p.Gly12Val)			
<u>115</u>	54	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.524G>A (p.Arg175His)			
<u>116</u>	51	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.451C>T (p.Pro151Ser) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1%	negative  TC<1%, IC<1%	3,81	MSS
<u>117</u>	-	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.818G>T (p.Arg273Leu) Microsatellite Instability (MSI):MSS		5,79	MSS
<u>118</u>	53	Female	KRAS:c.35G>A (p.Gly12Asp) HNF1A:c.864del G (p.Pro291GlnfsTer51) TP53:c. 78delT (p.Pro27LeufsTer17) Microsat ellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% ERCC1:Low expression TYMS:Low expression UGT1A1:HETEROZ YGOUS (6/7) DPD:WT	negative  TC<1%, IC<1%	6,1	MSS
<u>119</u>	68	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.332T>A (p.Leu111Gln)		7,26	

<u>120</u>	58	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:- TC 30%, IC 2%  Tumor Mutational Burden (TMB):5,08 Muts/MB	-  TC 30%, IC 2%	5,08	MSS
<u>121</u>	-	Male	ALK:c.3452C>T (p.Thr1151Met)  ATM:c.7916d elA (p.Lys2639ArgfsTer7)  FGFR4:c .749_768delinsGGA (p.Ile250Argfs*57)			
<u>122</u>	78	Female	KRAS:c.35G>A (p.Gly12Asp)  Tumor Mutational Burden (TMB):14,58 Muts/MB		14,58	
<u>123</u>	32	Male	KRAS:c.35G>T (p.Gly12Val)  NF2:c.1321delG (p.Ala441LeufsTer14)  Micros atellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):2,9 Muts/MB		2,9	MSS
<u>124</u>	62	Male	KRAS:c.35G>A (p.Gly12Asp)  MUTYH:c.536A> G (p.Tyr179Cys)  Microsatellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):2.03 Muts/MB		2,03	MSS
<u>125</u>	53	Male	KRAS:c.34G>C (p.Gly12Arg)  TP53:c.614A>G (p.Tyr205Cys)  Microsatellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):3.86 Muts/MB		3,86	MSS

<u>126</u>	66	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.742C>T (p.Arg248Trp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):13.03 Muts/MB	negative  TC<1%, IC<1%	13,03	MSS
<u>127</u>	77	Male	ATM:c.3673C>T (p.Gln1225Ter) BRCA2:c.8174 G>A (p.Trp2725Ter) CDKN2A:c.13 0delT (p.Tyr44ThrfsTer9) PALB2:c.2 761C>T (p.Gln921Ter) POLE:c.3038G> A (p.Trp1013Ter) STK11:c.1111 C>T (p.Gln371Ter) STK11:c.1111C >T (p.Gln371Ter) RAD50:c.2821C >T (p.Gln941Ter)			
<u>128</u>	65	Male	KRAS:c.183A>C (p.Gln61His)			
<u>129</u>	70	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.646G>A (p.Val216Met) MAP2K7:c.745 delA (p.Ile249SerfsTer162) AR:am plification CCNE1:amplificatio n Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):5.82 Muts/MB	negative  TC<1%, IC<1%	5,82	MSS
<u>130</u>	37	Female	KRAS:c.35G>A (p.Gly12Asp)			

<u>131</u>	66	Male	PALB2:c.2747_2748+4delAGG TAA Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC <1%, IC<1%  Tumor Mutational Burden (TMB):3.84 Muts/MB	negative  TC <1%, IC<1%	3,84	MSS
<u>132</u>	70	Male	SF3B1:c.1998G>C (p.Lys666Asn) DSC3:c.2503C>T (p.Arg835Ter) Microsatellite Instability (MSI):MSS PD-L1 expression: TC<1%, IC<1% Tumor Mutational Burden (TMB):9.4 Muts/MB	unknown negative  TC<1%, IC<1%	9,4	MSS
<u>133</u>	72	Female	KRAS:c.35G>A (p.Gly12Asp) CDKN2A:c.381_435delACGGTACCTGCGCGCG GCTGCGGGGGGACCAGAGGC AGTAACCATGCCGCATA (p.Arg128MetfsTer9) Microsa tellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):9.59 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1%, IC<1%	9,59	MSS
<u>134</u>	83	Male	MET:amplification			
<u>135</u>	65	Male	KRAS:c.35G>A (p.Gly12Asp) GNAS:c.601C>T (p.Arg201Cys) PD-L1 expression: TC<1%, IC=2 Tumor Mutational Burden (TMB):6.9 Muts/MB	unknown positive  TC<1%, IC=2	6,9	

<u>136</u>	52	Male	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):9.52 Muts/MB	negative  TC<1% IC<1%	9,52	MSS
<u>137</u>	79	Female	KRAS:c.772G>A (p.Glu258Lys) TP53:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC>50%, IC<1% Tumor Mutational Burden (TMB):4,78 Muts/MB ERCC1:Low expression TYMS:Low expression	positive  TC>50%, IC<1%	4,78	MSS
<u>138</u>	77	Male	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,87 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1%, IC<1%	3,87	MSS
<u>139</u>	57	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.702C>G (p.Tyr234Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC>50%, IC<1% Tumor Mutational Burden (TMB):4,92 Muts/MB ERCC1:High expression TYMS:Low expression	positive  TC>50%, IC<1%	4,92	MSS
<u>140</u>	51	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.856G>A (p.Glu286Lys)			

<u>141</u>	81	Female	KRAS:c.35G>T (p.Gly12Val)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):3,82 Muts/MB	negative  TC<1% IC<1%	3,82	MSS
<u>142</u>	50	Male	Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):3,81 Muts/MB  ERCC1:High expression  TYMS:Low expression	negative  TC<1% IC<1%	3,81	MSS
<u>143</u>	63	Female	KRAS:c.35G>A (p.Gly12Asp)  MDM2:amplification  Tumor Mutational Burden (TMB):5,94 Muts/MB		5,94	
<u>144</u>	51	Female	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.586C>T (p.Arg196Ter)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):21,85 Muts/MB  ERCC1:Low expression  TYMS:Low expression	negative  TC<1% IC<1%	21,85	MSS
<u>145</u>	58	Male	KRAS:c.35G>T (p.Gly12Val)  CDKN2A:c.138delIG (p.Arg47GlyfsTer6)  TP53:c.827C>A (p.Ala276Asp)			

<u>146</u>	63	Female	KRAS:c.34G>C (p.Gly12Arg)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):2,92 Muts/MB  ERCC1:High expression  TYMS:Low expression	negative  TC<1% IC<1%	2,92	MSS
<u>147</u>	71	Female	KRAS:c.35G>T (p.Gly12Val)  TP53:c.796G>T (p.Gly266Ter)  ATR:c.5605C>T (p.Gln1869Ter)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 30%, IC<1%  Tumor Mutational Burden (TMB): Muts/MB  ERCC1:Low expression  TYMS:Low expression	positive  TC 30%, IC<1%		MSS
<u>148</u>	64	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):6,77 Muts/MB	negative  TC<1% IC<1%	6,77	MSS
<u>149</u>	66	Male	KRAS:c.35G>T (p.Gly12Val)  TP53:c.743G>A (p.Arg248Gln)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 2%, IC<1%  Tumor Mutational Burden (TMB):5,76 Muts/MB	positive  TC 2%, IC<1%	5,76	MSS

<u>150</u>	49	Female	KRAS:c.34G>C (p.Gly12Arg)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 30% IC 1%  Tumor Mutational Burden (TMB):12,39 Muts/MB	positive  TC 30% IC 1%	12,39	MSS
<u>151</u>	62	Female	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.919+2T>G (splicing)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 30%, IC<1%  Tumor Mutational Burden (TMB):1,91 Muts/MB	positive  TC 30%, IC<1%	1,91	MSS
<u>152</u>	70	Female	KRAS:c.182A>G (p.Gln61Arg)		7,01	
<u>153</u>	72	Female	KRAS:c.35G>T (p.Gly12Val)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):14,29 Muts/MB  ERCC1:Low expression  TYMS:Low expression	negative  TC<1% IC<1%	14,29	MSS
<u>154</u>	50	Male	KRAS:c.35G>A (p.Gly12Asp)  CDKN2A:c.238C>T (p.Arg80Ter)  TP53:c.742C>T (p.Arg248Trp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC<1%, IC 5%  Tumor Mutational Burden (TMB):4,78 Muts/MB	positive  TC<1%, IC 5%	4,78	MSS

<u>155</u>	57	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.742C>T (p.Arg248Trp) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1 IC2% Tumor Mutational Burden (TMB):0,95 Muts/MB	positive T C<1 IC2%	0,95	MSS
<u>156</u>	74	Male	KRAS:c.183A>C (p.Gln61His) NOTCH1:c.2047 G>A (p.Ala683Thr) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,89 Muts/MB	negative  TC<1% IC<1%	3,89	MSS
<u>157</u>	55	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.421T>C (p.Cys141Arg) CDKN2A:c.262 G>T (p.Glu88Ter) SMAD4:c.719_7 20insT (p.Ala241SerfsTer23) Microsa tellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):7,71 Muts/MB	negative  TC<1%, IC<1%	7,71	MSS
<u>158</u>	57	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.524G>A (p.Arg175His) KRAS:amplifica tion Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):1,89 Muts/MB	negative  TC<1%, IC<1%	1,89	MSS

<u>159</u>	74	Female	KRAS:c.34G>C (p.Gly12Arg)  RSPO2 fusion:EIF3E(1) - RSPO2(2)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):5,87 Muts/MB	negative  TC<1% IC<1%	5,87	MSS
<u>160</u>	61	Male	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.402T>G (p.Phe134Leu)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC<1%, IC 30%  Tumor Mutational Burden (TMB):4,8 Muts/MB	positive  T C<1%, IC 30%	4,8	MSS
<u>161</u>	63	Male	KRAS:c.35G>T (p.Gly12Val)  TP53:c.599+2T> G ()  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 2%, IC<1%  Tumor Mutational Burden (TMB):3,84 Muts/MB	positive  T C 2%, IC<1%	3,84	MSS
<u>162</u>	41	Male	KRAS:c.34G>C (p.Gly12Arg)  TP53:c.856G>A (p.Glu286Lys)  SMAD4:c.1333 C>T (p.Arg445Ter)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):6,76 Muts/MB	negative  TC<1% IC<1%	6,76	MSS
<u>163</u>	78	Male	ATM:c.5980A>T (p.Lys1994Ter)  KRAS:c.34G>C (p.Gly12Arg)			

<u>164</u>	67	Female	KRAS:c.35G>T (p.Gly12Val) RNF43:c.1418del G (p.Gly473AlafsTer29) TP53:c. 586C>T (p.Arg196Ter)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC<1%, IC 10% Tumor Mutational Burden (TMB):5,78 Muts/MB	positive  T C<1%, IC 10%	5,78	MSS
<u>165</u>	62	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 10%, IC<1% Tumor Mutational Burden (TMB):7,73 Muts/MB  ERCC1:Low expression  TYMS:Low expression	positive  T C 10%, IC<1%	7,73	MSS
<u>166</u>	69	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.817C>T (p.Arg273Cys)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 20%, IC 10% Tumor Mutational Burden (TMB):4,88 Muts/MB	positive  T C 20%, IC 10%	4,88	MSS
<u>167</u>	60	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 5% IC 15% Tumor Mutational Burden (TMB):0,96 Muts/MB	positive  T C 5% IC 15%	0,96	MSS

<u>168</u>	73	Male	KRAS:c.183A>T (p.Gln61His) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,83 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	negative  TC<1%, IC<1%	4,83	MSS
<u>169</u>	82	Female	BRCA1:c.5251C>T (p.Arg1751Ter) KRAS:c.35G>A (p.Gly12Asp) TP53:c.687T>A (p.Cys229Ter) RASA2:c.2023delC (p.Gln675LysfsTer2) AR:amplification SLCO1B3:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC 10% IC<1% Tumor Mutational Burden (TMB):6,7 Muts/MB	positive  TC 10% IC<1%	6,7	MSS
<u>170</u>	58	Male	KRAS:c.35G>A (p.Gly12Asp) STK11:c.180C>G (p.Tyr60Ter) STK11:c.180C>G (p.Tyr60Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,29 Muts/MB	negative  TC<1%, IC<1%	4,29	MSS

<u>171</u>	80	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.841G>A (p.Asp281Asn) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):1,93 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:HETEROZ YGOUS (6/7) DPD:WT	negative  TC<1%, IC<1%	1,93	MSS
<u>172</u>	71	Male	CDKN2A:c.186_187insG (p.Leu63AlafsTer57) ATM:c.9 023G>A (p.Arg3008His) KRAS:c.35G>A (p.Gly12Asp) RNF43:c.714G> A (p.Trp238Ter) CDK2:amplifica tion			
<u>173</u>	64	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His) CDKN2A:c.172 C>T (p.Arg58Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,84 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	negative  TC<1%, IC<1%	4,84	MSS

<u>174</u>	51	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):0,96 Muts/MB	negative  TC<1%, IC<1%	0,96	MSS
<u>175</u>	58	Female	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.818G>A (p.Arg273His)  Microsatellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):12,7 Muts/MB		12,7	MSS
<u>176</u>	65	Male	KRAS:c.35G>A (p.Gly12Asp)  SMAD4:c.353C>T (p.Ala118Val)  RSPO2 fusion:EIF3E(1) - RSPO2(2)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):6,87 Muts/MB	negative  TC<1%, IC<1%	6,87	MSS
<u>177</u>	57	Male	KRAS:c.35G>T (p.Gly12Val)  TP53:c.743G>A (p.Arg248Gln)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):4,79 Muts/MB  ERCC1:Low expression  TYMS:Low expression	negative  TC<1%, IC<1%	4,79	MSS
<u>178</u>	54	Female	KRAS:c.35G>T (p.Gly12Val)  TP53:c.916C>T (p.Arg306Ter)  CDKN2A:c.233_234insT (p.Thr79fs)			

<u>179</u>	63	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):32,89 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1%, IC<1%	32,89	MSS
<u>180</u>	66	Female	KRAS:c.34G>C (p.Gly12Arg) SMAD4:c.175del A (p.Thr59GlnfsTer3) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2,86 Muts/MB	negative  TC<1% IC<1%	2,86	MSS
<u>181</u>	71	Male	KRAS:c.34G>C (p.Gly12Arg) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):5,72 Muts/MB	negative  TC<1% IC<1%	5,72	MSS
<u>182</u>	64	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.701A>G (p.Tyr234Cys)			
<u>183</u>	59	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.637C>T (p.Arg213Ter) AR:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,81 Muts/MB	negative  TC<1% IC<1%	3,81	MSS

<u>184</u>	62	Female	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC<1%, IC 2%  Tumor Mutational Burden (TMB):10,29 Muts/MB	positive  T C<1%, IC 2%	10,29	MSS
<u>185</u>	60	Male	KRAS:c.35G>A (p.Gly12Asp)  CDKN2A:c.47_5 0delTGGC (p.Leu16ProfsTer9)  TP53:c.83 3C>T (p.Pro278Leu)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC<1%, IC 15%  Tumor Mutational Burden (TMB):7,81 Muts/MB	positive  T C<1%, IC 15%	7,81	MSS
<u>186</u>	43	Female				
<u>187</u>	51	Male	Microsatellite Instability (MSI):-  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB): Muts/MB	negative  TC<1% IC<1%		-

<u>188</u>	66	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.659A>G (p.Tyr220Cys) GNAS:c.602G>A (p.Arg201His) STED2:c.2324_2325delTT (p.Val775Glu>Ter5) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2,9 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1% IC<1%	2,9	MSS
<u>189</u>	36	Female	Microsatellite Instability (MSI):MSS PD-L1 expression:negative  Tumor Mutational Burden (TMB):0,96 Muts/MB	negative	0,96	MSS
<u>190</u>	58	Female	KRAS:c.34G>C (p.Gly12Arg) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):1,92 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:HETEROZYGOUS (6/7) DPD:WT	negative  TC<1% IC<1%	1,92	MSS

<u>191</u>	55	Male	BRCA2:c.3374_3375delTT (p.Phe1125Ter) CDKN2A:c.131_132insA (p.Tyr44Ter) KRAS:c.35G>A (p.Gly12Asp) PIK3CA:c.1358A>G (p.Glu453Gly) TP53:c.817C>T (p.Arg273Cys) FBXW7:c.1393C>T (p.Arg465Cys) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):7,33 Muts/MB ERCC1:Low expression TYMS:Low expression	negative TC<1%, IC<1%	7,33	MSS
<u>192</u>	60	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.646G>A (p.Val216Met) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):4,12 Muts/MB ERCC1:High expression TYMS:Low expression	negative TC<1% IC<1%	4,12	MSS
<u>193</u>	79	Female	KRAS:c.34G>A (p.Gly12Ser) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,82 Muts/MB ERCC1:Low expression TYMS:Low expression	negative TC<1%, IC<1%	4,82	MSS

<u>194</u>	68	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):1,98 Muts/MB	negative  TC<1%, IC<1%	1,98	MSS
<u>195</u>	65	Male	TP53:c.997delC (p.Arg333ValfsTer12)			
<u>196</u>	49	Female	ATM:c.8545C>T (p.Arg2849Ter) ATM:c.1564G >T (p.Glu522Ter) KRAS:c.35G>A (p.Gly12Asp) SMAD4:c.403C> T (p.Arg135Ter) RNF43:c.1436_ 1437delTG (p.Val479GlyfsTer25) PIK3CA: c.263G>A (p.Arg88Gln) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC 50%,IC 5% Tumor Mutational Burden (TMB):9,55 Muts/MB ERCC1:Low expression TYMS:Low expression	positive T C 50%,IC 5%	9,55	MSS
<u>197</u>	73	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.743G>A (p.Arg248Gln) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):4,82 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1% IC<1%	4,82	MSS

<u>198</u>	60	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.742C>T (p.Arg248Trp) MYC:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2,98 Muts/MB	negative  TC<1% IC<1%	2,98	MSS
<u>199</u>	60	Female	KRAS:c.34G>C (p.Gly12Arg) SMAD4:c.362T>A (p.Leu121Ter) TP53:c.817C>T (p.Arg273Cys) FGF23:amplification CCND2:amplification Microsatellite Instability (MSI):MSS Tumor Mutational Burden (TMB):8,61 Muts/MB		8,61	MSS
<u>200</u>	82	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.710T>A (p.Met237Lys) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,99 Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	negative  TC<1% IC<1%	3,99	MSS

<u>201</u>	43	Female	TP53:c.679_690delTCTGACTG TACC (p.Ser227_Thr230del) MET:amplification MRE11:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):9,8 Muts/MB ERCC1:High expression TYMS:Low expression	negative  TC<1% IC<1%	9,8	MSS
<u>202</u>	77	Male	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):1,96 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1% IC<1%	1,96	MSS
<u>203</u>	81	Male	KRAS:c.35G>T (p.Gly12Val) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,97 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1% IC<1%	3,97	MSS
<u>204</u>	76	Male	ERBB2:c.2524G>A (p.Val842Ile) SMAD4:c.1082G>A (p.Arg361His) TP53:c.824G>A (p.Cys275Tyr) KRAS:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):6,76 Muts/MB	negative  TC<1% IC<1%	6,76	MSS

<u>205</u>	51	Male	BRCA2:c.67+1G>A KRAS:c.35 G>T (p.Gly12Val) TP53:c.817C>T (p.Arg273Cys) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB): Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:HOMOZY GOYS MUTATED (7/7) DPD:WT	negative  TC<1% IC<1%		MSS
<u>206</u>	63	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):4,78 Muts/MB	negative  TC<1% IC<1%	4,78	MSS
<u>207</u>	49	Female	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):2,87 Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	negative  TC<1%, IC<1%	2,87	MSS

<u>208</u>	39	Female	KRAS:c.35G>T (p.Gly12Val) SMAD4:c.403C>T (p.Arg135Ter) RB1:c.1351_1357delCGCTTGT (p.Arg451IlefsTer4) TP53:c.985_993+4delACCTTCAGGTAC (splicing) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,89 Muts/MB	negative  TC<1% IC<1%	3,89	MSS
<u>209</u>	42	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.159G>A (p.Trp53Ter)			
<u>210</u>	70	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2,86 Muts/MB	negative  TC<1% IC<1%	2,86	MSS
<u>211</u>	64	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.403T>C (p.Cys135Arg) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):2,85 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1%, IC<1%	2,85	MSS

<u>212</u>	66	Male	BAP1:c.125delC (p.Pro42LeufsTer30) KRAS:c.183A>T (p.Gln61His) ARID1A:c.2180_2189del (p.Arg727LeufsTer12) ERCC2:c.1972C>T (p.Arg658Cys) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):5,3 Muts/MB ERCC1:High expression TYMS:Low expression	negative TC<1% IC<1%	5,3	MSS
<u>213</u>	59	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.844C>T (p.Arg282Trp) DPYD:c.1905+1G>A Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):7,58 Muts/MB	negative TC<1% IC<1%	7,58	MSS
<u>214</u>	58	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.659A>G (p.Tyr220Cys) EMSY:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1% IC 2% Tumor Mutational Burden (TMB):7,6 Muts/MB ERCC1:High expression TYMS:Low expression	positive TC<1% IC 2%	7,6	MSS

<u>215</u>	74	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.646G>A (p.Val216Met) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1% IC 10% Tumor Mutational Burden (TMB):4,77 Muts/MB ERCC1:Low expression RRM1:Low expression UGT1A1:WT (6/6) DPD:WT	positive TC<1% IC 10%	4,77	MSS
<u>216</u>	67	Male	KRAS:c.34G>C (p.Gly12Arg) SMAD4:c.1081C>T (p.Arg361Cys)			
<u>217</u>	64	Male	ALK fusion:HIP1(30) - ALK(20) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,79 Muts/MB	negative TC<1% IC<1%	3,79	MSS
<u>218</u>	73	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,85 Muts/MB	negative TC<1%, IC<1%	3,85	MSS
<u>219</u>	57	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.510_517 delinsA (p.Glu171Ter) TP53:c.759_761delCAT (p.Ile255del)			
<u>220</u>	73	Female	KRAS:c.436G>A (p.Ala146Thr)			

<u>221</u>	59	Male	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,81 Muts/MB	negative  TC<1%, IC<1%	3,81	MSS
<u>222</u>	74	Male	KRAS:c.35G>T (p.Gly12Val)			
<u>223</u>	82	Female	MUTYH:c.1012C>T (p.Gln338Ter) IDH2:c.514A>T (p.Arg172Trp) BAP1:c.1123G>T (p.Glu375Ter) PIK3R1:c.1690A>G (p.Asn564Asp) TP53:c.374C>A (p.Thr125Lys) EIF1AX:amplification SOS1:amplification STAG2:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):9,39 Muts/MB	negative  TC<1%, IC<1%	9,39	MSS
<u>224</u>	51	Male	Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2,85 Muts/MB	negative  TC<1% IC<1%	2,85	MSS

<u>225</u>	52	Female	KRAS:c.35G>T (p.Gly12Val)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 30,51%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):17,96 Muts/MB  ERCC1:Low expression  TYMS:Low expression	negative  TC<1%, IC<1%	17,96	MSS
<u>226</u>	67	Male	PTEN:c.517C>T (p.Arg173Cys)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):3,82 Muts/MB	negative  TC<1%, IC<1%	3,82	MSS
<u>227</u>	45	Male	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.637C>T (p.Arg213Ter)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):2,17 Muts/MB	negative  TC<1%, IC<1%	2,17	MSS
<u>228</u>	63	Female	KRAS:c.35G>T (p.Gly12Val)  TP53:c.524G>A (p.Arg175His)  Microsatellite Instability (MSI):MSS  PD-L1 expression:-   Tumor Mutational Burden (TMB):6,74 Muts/MB	-	6,74	MSS

<u>229</u>	59	Female	CDKN2A:c.233_234delTC (p.Leu78HisfsTer41) KRAS:c.3 4G>C (p.Gly12Arg) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):0,97 Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	negative  TC<1%, IC<1%	0,97	MSS
<u>230</u>	62	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.559+1G> A ( ) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 3,64% PD-L1 expression:positive TC<1% IC 2% Tumor Mutational Burden (TMB):4,93 Muts/MB	positive T C<1% IC 2%	4,93	MSS

<u>231</u>	49	Female	TP53:c.1001G>T (p.Gly334Val)  BRAF fusion:CCNY(1) - BRAF(10)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 28,13%  PD-L1 expression:positive TC<1%, IC 10%  Tumor Mutational Burden (TMB):3,84 Muts/MB  ERCC1:Low expression  TYMS:Low expression  UGT1A1:HOMOZYGOUS MUTATED (7/7)  DPD:WT	positive  TC<1%, IC 10%	3,84	MSS
<u>232</u>	57	Male	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.587G>C (p.Arg196Pro)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 23,21%  PD-L1 expression:positive TC<1% IC 10%  Tumor Mutational Burden (TMB):7,59 Muts/MB  ERCC1:High expression  TYMS:Low expression	positive  TC<1% IC 10%	7,59	MSS

<u>233</u>	70	Female	KRAS:c.35G>T (p.Gly12Val)  TP53:c.743G>A (p.Arg248Gln)  PIK3CA:amplification  MECOM:amplification  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 10,09%  PD-L1 expression:positive TC<1%, IC 2%  Tumor Mutational Burden (TMB):4,79 Muts/MB	positive  TC<1%, IC 2%	4,79	MSS
<u>234</u>	73	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):4,78 Muts/MB	negative  TC<1%, IC<1%	4,78	MSS
<u>235</u>	73	Male	KRAS:c.34G>C (p.Gly12Arg)  CCND3:amplification  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 43,49%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):5,75 Muts/MB	negative  TC<1%, IC<1%	5,75	MSS
<u>236</u>	56	Female	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):0,98 Muts/MB	negative  TC<1% IC<1%	0,98	MSS

<u>237</u>	70	Male	BLM:c.1720_1735del (p.Ala575ProfsTer38)  KRAS:c.35G>A (p.Gly12Asp)  NOTCH2:amplification  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 7,63  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):1,94 Muts/MB	negative  TC<1% IC<1%	1,94	MSS
<u>238</u>	66	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 7,75%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):1,9 Muts/MB	negative  TC<1%, IC<1%	1,9	MSS
<u>239</u>	68	Female	AMER1:c.1138G>T (p.Glu380Ter)  KRAS:c.35G>A (p.Gly12Asp)  TP53:c.602delT (p.Leu201CysfsTer46)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 20%, IC 15%  Tumor Mutational Burden (TMB):4 Muts/MB	positive  TC 20%, IC 15%	4	MSS

<u>240</u>	48	Male	KRAS:c.35G>T (p.Gly12Val)  TP53:c.524G>A (p.Arg175His)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):4,95 Muts/MB  ERCC1:High expression  TYMS:Low expression  UGT1A1:HETEROZ YGOUS (6/7)  DPD:WT	negative  TC<1% IC<1%	4,95	MSS
<u>241</u>	75	Female	KRAS:c.35G>T (p.Gly12Val)  TP53:c.818G>A (p.Arg273His)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):1,95 Muts/MB	negative  TC<1% IC<1%	1,95	MSS
<u>242</u>	80	Male	KRAS:c.35G>C (p.Gly12Ala)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):0,97 Muts/MB  ERCC1:High expression  TYMS:Low expression	negative  TC<1% IC<1%	0,97	MSS
<u>243</u>	59	Female	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):4,77 Muts/MB	negative  TC<1%, IC<1%	4,77	MSS

<u>244</u>	41	Male	HRAS:c.351G>T (p.Lys117Asn) ATRX:c.3200C>A (p.Ser1067Ter) NOTCH4:c.1845C>A (p.Cys615Ter) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 66,58% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):12,41 Muts/MB	negative TC<1%, IC<1%	12,41	MSS
<u>245</u>	69	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.470T>A (p.Val157Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):2,85 Muts/MB	negative TC<1%, IC<1%	2,85	MSS
<u>246</u>	49	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC 2% IC 10% Tumor Mutational Burden (TMB):2.98 Muts/MB	positive TC 2% IC 10%	2,98	MSS
<u>247</u>	42	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):7,2 Muts/MB	negative TC<1% IC<1%	7,2	MSS

<u>248</u>	60	Female	BRCA2:c.7868A>G (p.His2623Arg) NBN:c.2140C>T (p.Arg714Ter) SMAD4:c.1140-2A>T (splicing) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 34,47 PD-L1 expression:negative TC<1% , IC<1% Tumor Mutational Burden (TMB): 6.63 Muts/MB	negative TC<1% , IC<1%	6,63	MSS
<u>249</u>	77	Female	KRAS:c.35G>A (p.Gly12Asp) RAD50:c.326_329delCAGA (p.Thr109AsnfsTer20) ATM:c.5497-2A>G			
<u>250</u>	56	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.766_767insA (p.Thr256AsnfsTer8) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,83 Muts/MB	negative TC<1% IC<1%	3,83	MSS
<u>251</u>	40	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.817C>T (p.Arg273Cys) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,8 Muts/MB	negative TC<1% IC<1%	3,8	MSS

<u>252</u>	50	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.701A>G (p.Tyr234Cys) RB1:c.248delC (p.Ser83LeufsTer28) PTPRT:c. 1843C>T (p.Gln615Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative  Tumor Mutational Burden (TMB):1,9 Muts/MB ERCC1:High expression TYMS:Low expression	negative	1,9	MSS
<u>253</u>	46	Male	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):6,65 Muts/MB ERCC1:High expression TYMS:Low expression	negative  TC<1% IC<1%	6,65	MSS
<u>254</u>	68	Male	RAD51C:c.706- 2A>G KRAS:c.35G>A (p.Gly12Asp) DDR1:c.1039C> T (p.Gln347Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,8 Muts/MB	negative  TC<1% IC<1%	3,8	MSS

<u>255</u>	81	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.743G>A (p.Arg248Gln) MGA:c.6984_6 987delTGAG (p.Ser2328ArgfsTer6) CDKN2 B fusion:MTAP(5) - CDKN2B- AS1-004(5) PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3,82 Muts/MB	negative  TC<1% IC<1%	3,82	
<u>256</u>	72	Female				
<u>257</u>	70	Male	KRAS:c.35G>T (p.Gly12Val) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):6,22 Muts/MB	negative  TC<1%, IC<1%	6,22	MSS
<u>258</u>	71	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.310C>T (p.Gln104Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,49 Muts/MB	negative  TC<1%, IC<1%	4,49	MSS

<u>259</u>	65	Male	KRAS:c.35G>A (p.Gly12Asp)  UGT1A1:c.211G>A (p.Gly71Arg)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive IC 15%, TC<1%  Tumor Mutational Burden (TMB):1,27 Muts/MB  ERCC1:High expression  TYMS:Low expression	positive  IC 15%, TC<1%	1,27	MSS
<u>260</u>	55	Male	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.159_160insG (p.Phe54ValfsTer3)			
<u>261</u>	69	Female	KRAS:c.35G>T (p.Gly12Val)  TP53:c.89dupA (p.Asn30LysfsTer13)  Microsatellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):4,77 Muts/MB		4,77	MSS
<u>262</u>	66	Female	KRAS:c.183A>T (p.Gln61His)  ERBB2:amplification  KRAS:amplification  NTRK3:amplification  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 12,33%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):4,79 Muts/MB  ERCC1:High expression  TYMS:Low expression  UGT1A1:HETEROZYGOUS (6/7)  DPD:WT	negative  TC<1%, IC<1%	4,79	MSS

<u>263</u>	67	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.713G>T (p.Cys238Phe) Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 9,41% PD-L1 expression:positive TC 2%, IC<1% Tumor Mutational Burden (TMB):1,99 Muts/MB	positive T C 2%, IC<1%	1,99	MSS
<u>264</u>	64	Male	KRAS:c.34G>C (p.Gly12Arg) SMAD4:c.1333C >T (p.Arg445Ter) CDKN2A:c.196 delC (p.His66ThrfsTer80) TP53:c.1 12C>T (p.Gln38Ter) IKBKB:amplificat ion Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):5.71 Muts/MB	negative  TC<1% IC<1%	5,71	MSS
<u>265</u>	57	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.602_603 insT (p.Leu201PhefsTer8) CCNE1:a mplification AKT2:amplificati on AXL:amplification Microsa tellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 1.64 % PD-L1 expression:negative TC <1% IC <1% Tumor Mutational Burden (TMB):1.9 Muts/MB	negative  TC <1% IC <1%	1,9	MSS

<u>266</u>	63	Male	KRAS:c.35G>A (p.Gly12Asp) BCOR:c.3649C>T (p.Arg1217Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1%, IC 5% Tumor Mutational Burden (TMB):5,83 Muts/MB	positive T C<1%, IC 5%	5,83	MSS
<u>267</u>	62	Male	NF1:c.5881A>T (p.Lys1961Ter) PTPN11:c.205 G>A (p.Glu69Lys)			
<u>268</u>	62	Female	KRAS:c.35G>A (p.Gly12Asp) MSH3:c.2319- 1G>A (splicing) ARID1A:c.4360C>T (p.Gln1454Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):4.82 Muts/MB	negative  TC<1% IC<1%	4,82	MSS
<u>269</u>	78	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.817C>T (p.Arg273Cys) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC 2%, IC<1% Tumor Mutational Burden (TMB):2,91 Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	positive T C 2%, IC<1%	2,91	MSS
<u>270</u>	65	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.743G>A (p.Arg248Gln)			

<u>271</u>	76	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):1.91 Muts/MB	negative  TC<1% IC<1%	1,91	MSS
<u>272</u>	75	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.920-1G>A (splicing)			
<u>273</u>	54	Male	KRAS:c.35G>T (p.Gly12Val) MUTYH:c.89delC (p.Ala30GlufsTer28) TP53:c.742C>T (p.Arg248Trp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB): 2.89 Muts/MB	negative  TC<1% IC<1%	2,89	MSS
<u>274</u>	41	Male	KRAS:c.35G>A (p.Gly12Asp) SMAD4:c.250-2A>G ( ) SMARCA4:c.4620_4627del GAAGATAA (p.Lys1541GlyfsTer37)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 25,42% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,82 Muts/MB	negative  TC<1%, IC<1%	3,82	MSS
<u>275</u>	79	Male	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3.14 Muts/MB	negative  TC<1% IC<1%	3,14	MSS

<u>276</u>	47	Male	KRAS:c.183A>C (p.Gln61His) TP53:c.844C>T (p.Arg282Trp) CDH1:c.1565+1 G>A ( ) CDH1:c.1320+1G>T ( ) KDM6A:c.737delT (p.Leu246TyrfsTer4) Microsat ellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,18 Muts/MB	negative  TC<1%, IC<1%	3,18	MSS
<u>277</u>	59	Female	KRAS:c.34G>C (p.Gly12Arg) ARID1A:c.31_56 del (p.Ser11AlafsTer91) KDR:c.10 62C>A (p.Tyr354Ter) TP53:c.743G>A (p.Arg248Gln) FANCG:amplifi cation Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):2.92 Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:HETEROZ YGOUS (6/7) DPD:WT	negative  TC <1% IC<1%	2,92	MSS
<u>278</u>	60	Male	KRAS:c.183A>C (p.Gln61His) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):7,02 Muts/MB	negative  TC<1%, IC<1%	7,02	MSS

<u>279</u>	72	Female	KRAS:c.34G>C (p.Gly12Arg)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):0,95 Muts/MB	negative  TC<1%, IC<1%	0,95	MSS
<u>280</u>	66	Female	KRAS:c.35G>C (p.Gly12Ala)  TP53:c.742C>T (p.Arg248Trp)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 36.49 %  PD-L1 expression:positive TC<1% IC 5%  Tumor Mutational Burden (TMB):1.89 Muts/MB	positive  T C<1% IC 5%	1,89	MSS
<u>281</u>	61	Female	KRAS:c.34G>C (p.Gly12Arg)  SMAD4:c.362T> A (p.Leu121Ter)  TP53:c.817C>T (p.Arg273Cys)  STAG2:c.1229 G>C (p.Cys410Ser)  ABRAXAS1:c.11 33_1134insCCCAGTAA (p.Gln379ProfsTer10)  Micros atellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 27,76  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):10,44 Muts/MB	negative  TC<1%, IC<1%	10,44	MSS

<u>282</u>	84	Female	KRAS:c.35G>A (p.Gly12Asp) DPYD:c.1905+1G>A TP53:c.817C>T (p.Arg273Cys) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 15,76% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,79 Muts/MB	negative TC<1%, IC<1%	3,79	MSS
<u>283</u>	62	Male	MRE11A:c.1252_1253insA (p.Ile418AsnfsTer39) KRAS:c.35G>T (p.Gly12Val) ID3:amplification MCL1:amplification ELF3:amplification H3-3A:amplification PCBP1:amplification H3C2:amplification H1-4:amplification PIM1:amplification MET:amplification FANCF:amplification CDKN1B:amplification KNSTRN:amplification GNA13:amplification H3-3B:amplification Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 42.67 % PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):2.85 Muts/MB	negative TC<1%, IC<1%	2,85	MSS

<u>284</u>	64	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 2.42 % PD-L1 expression:negative TC <1% IC<1%  Tumor Mutational Burden (TMB):0.95 Muts/MB	negative  TC <1% IC<1%	0,95	MSS
<u>285</u>	57	Female	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1%, IC 1% Tumor Mutational Burden (TMB):1,89 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:HOMOZY GOYS MUTATED (7/7) DPD:WT	positive T C<1%, IC 1%	1,89	MSS
<u>286</u>	58	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.824G>A (p.Cys275Tyr) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 7,61% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):2,85 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:HETEROZ YGOUS (6/7) DPD:WT	negative  TC<1%, IC<1%	2,85	MSS

<u>287</u>	58	Female	KRAS:c.35G>A (p.Gly12Asp) RAD50:c.326_329delCAGA (p.Thr109AsnfsTer20)			
<u>288</u>	52	Female	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):6,62 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:HETEROZ YGOUS (6/7) DPD:WT	negative  TC<1%, IC<1%	6,62	MSS
<u>289</u>	50	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.808T>C (p.Phe270Leu) FGFR3 fusion:FGFR3-TACC3 Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 8,65% PD-L1 expression:positive TC 30%, IC 5% Tumor Mutational Burden (TMB):2,85 Muts/MB	positive  TC 30%, IC 5%	2,85	MSS
<u>290</u>	79	Male	PIK3CA:c.1633G>A (p.Glu545Lys)			

<u>291</u>	58	Female	KRAS:c.35G>T (p.Gly12Val) RNF43:c.1204C>T (p.Gln402Ter) TP53:c.455C>T (p.Pro152Leu) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 5.33 % PD-L1 expression:negative TC <1% IC<1%  Tumor Mutational Burden (TMB):1.91 Muts/MB	negative  TC <1% IC<1%	1,91	MSS
<u>292</u>	56	Male	NBN:c.654_658delAAAAC (p.Lys219AsnfsTer16) FGFR1: c.1731C>G (p.Asn577Lys) TERT:amplifica tion Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 62,57% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,8 Muts/MB	negative  TC<1%, IC<1%	3,8	MSS
<u>293</u>	65	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.380C>T (p.Ser127Phe) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 13.64 % PD-L1 expression:negative TC <1% IC<1%  Tumor Mutational Burden (TMB):2.85 Muts/MB	negative  TC <1% IC<1%	2,85	MSS

<u>294</u>	59	Female	KRAS:c.34G>C (p.Gly12Arg)  Microsatellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):0,95 Muts/MB		0,95	MSS
<u>295</u>	57	Male	KRAS:c.35G>A (p.Gly12Asp)  SMAD4:c.1096C >T (p.Gln366Ter)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 26,46%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):4,74 Muts/MB  ERCC1:High expression  TYMS:Low expression  UGT1A1:WT (6/6)  DPD:WT	negative  TC<1%, IC<1%	4,74	MSS
<u>296</u>	54	Male	KRAS:c.34G>T (p.Gly12Cys)  GNAS:c.602G>A (p.Arg201His)  ARID1A:c.1780 C>T (p.Gln594Ter)  NOTCH4:c.104 4delC (p.Gly349AlafsTer49)  Microsa tellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):4.76 Muts/MB		4,76	MSS

<u>297</u>	57	Female	KRAS:c.183A>C (p.Gln61His) TP53:c.378C>G (p.Tyr126Ter) H3C2:amplification Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,73 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	negative TC<1%, IC<1%	4,73	MSS
<u>298</u>	59	Male	EPHA2:c.1969C>T (p.Arg657Ter) PIK3CA:c.3140 A>G (p.His1047Arg) MYC:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC 2%, IC<1% Tumor Mutational Burden (TMB):5,69 Muts/MB	positive TC 2%, IC<1%	5,69	MSS
<u>299</u>	74	Male	BARD1:c.947T>G (p.Leu316Ter) AMER1:c.1489 C>T (p.Arg497Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB): Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:HETEROZYGOUS (6/7) DPD:WT	negative TC<1% IC<1%		MSS

<u>300</u>	49	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His) SMAD4:c.133A >G (p.Lys45Glu) TGFB2:c.1232T >C (p.Leu411Pro) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 2,19% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,74 Muts/MB	negative  TC<1%, IC<1%	4,74	MSS
<u>301</u>	67	Female	TP53:c.158G>A (p.Trp53Ter) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 16,16% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,74 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1%, IC<1%	4,74	MSS
<u>302</u>	70	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.659A>G (p.Tyr220Cys) NCOR1:c.1519 C>T (p.Arg507Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1%, IC 3% Tumor Mutational Burden (TMB):2,84 Muts/MB	positive T C<1%, IC 3%	2,84	MSS

<u>303</u>	64	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.404G>A (p.Cys135Tyr) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC 1% IC <1%  Tumor Mutational Burden (TMB):3.79 Muts/MB ERCC1:High expression TYMS:Low expression	negative  TC 1% IC <1%	3,79	MSS
<u>304</u>	59	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.961A>T (p.Lys321Ter) SF3B1:c.2098A >G (p.Lys700Glu) AURKC:c.420de IA (p.Glu140AspfsTer7) MYC:am plification Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 32,66% PD-L1 expression:positive TC 2%, IC 1% Tumor Mutational Burden (TMB):2,85 Muts/MB ERCC1:High expression TYMS:Low expression	positive T C 2%, IC 1%	2,85	MSS
<u>305</u>	60	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.743G>A (p.Arg248Gln)			

<u>306</u>	78	Male	KRAS:c.182A>G (p.Gln61Arg) SF3B1:c.2098A>G (p.Lys700Glu) TP53:c.844C>T (p.Arg282Trp) BCL2L12:-  Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 38.87 % PD-L1 expression:positive TC 20% IC 5% Tumor Mutational Burden (TMB):3.79 Muts/MB	positive T C 20% IC 5%	3,79	MSS
<u>307</u>	76	Female	KRAS:c.35G>A (p.Gly12Asp) CDC73:c.131+1 G>T (splicing) RBM10:c.2661delA (p.Glu888LysfsTer24) CDKN1 A:c.206_207insCG (p.Leu71AlafsTer78) Microsat ellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:positive TC<1%, IC 5% Tumor Mutational Burden (TMB):5,71 Muts/MB	positive T C<1%, IC 5%	5,71	MSS
<u>308</u>	66	Female	ARID1B:c.1618C>T (p.Gln540Ter) Microsatellite Instability (MSI):MSS Tumor Mutational Burden (TMB):fail Muts/MB		fail	MSS

<u>309</u>	74	Female	KRAS:c.35G>T (p.Gly12Val)  TP53:c.711G>T (p.Met237Ile)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 37,87%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):0,95 Muts/MB	negative  TC<1%, IC<1%	0,95	MSS
<u>310</u>	52	Female	KRAS:c.35G>T (p.Gly12Val)  CDKN2A:c.150+1 G>T (splicing)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 9.58 %  PD-L1 expression:negative TC <1% IC<1%  Tumor Mutational Burden (TMB):2.84 Muts/MB	negative  TC <1% IC<1%	2,84	MSS
<u>311</u>	77	Female	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.722C>G (p.Ser241Cys)  SMAD4:c.1082 G>A (p.Arg361His)  CDKN2A:c.311 delT (p.Leu104ArgfsTer42)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0%  PD-L1 expression:positive TC 5%, IC<1%  Tumor Mutational Burden (TMB):4,75 Muts/MB	positive  TC 5%, IC<1%	4,75	MSS

<u>312</u>	37	Female	KRAS:c.35G>T (p.Gly12Val)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):11.7 Muts/MB  ERCC1:High expression  TYMS:Low expression  UGT1A1:HETEROZ YGOUS (6/7)  DPD:WT	negative  TC<1% IC<1%	11,7	MSS
<u>313</u>	73	Male	KRAS:c.35G>A (p.Gly12Asp)  FBXW7:c.1436G>A (p.Arg479Gln)  CREBBP:c.4232G>T (p.Gly1411Val)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):6,65 Muts/MB	negative  TC<1%, IC<1%	6,65	MSS
<u>314</u>	37	Male	Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 19.62 %  PD-L1 expression:negative TC <1%IC<1%  Tumor Mutational Burden (TMB):1.89 Muts/MB	negative  TC <1%IC<1%	1,89	MSS
<u>315</u>	53	Female	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.374C>A (p.Thr125Lys)  Microsatellite Instability (MSI):MSS  Tumor Mutational Burden (TMB):4.74 Muts/MB		4,74	MSS

<u>316</u>	74	Male	KRAS:c.35G>T (p.Gly12Val) TP53:c.342_343insG (p.His115AlafsTer34) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 1.59 % PD-L1 expression:positive TC 25% IC <1% Tumor Mutational Burden (TMB):5.69 Muts/MB	positive TC 25% IC <1%	5,69	MSS
<u>317</u>	57	Male				
<u>318</u>	54	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.592G>T (p.Glu198Ter) SMAD4:c.1051G>T (p.Asp351Tyr) Microsatellite Instability (MSI):MSS PD-L1 expression negative TC<1%, IC<1% Tumor Mutational Burden (TMB):1,9 Muts/MB	positive TC<1%, IC<1%	1,9	MSS
<u>319</u>	61	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.844C>T (p.Arg282Trp) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):1,9 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT	negative TC<1%, IC<1%	1,9	MSS

<u>320</u>	58	Female	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 5,52%  PD-L1 expression:positive TC 10%, IC 1%  Tumor Mutational Burden (TMB):5,7 Muts/MB	positive  TC 10%, IC 1%	5,7	MSS
<u>321</u>	79	Male	KRAS:c.35G>A (p.Gly12Asp)  TP53:c.587G>C (p.Arg196Pro)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 2,39%  PD-L1 expression:positive TC 10%, IC<1%  Tumor Mutational Burden (TMB):3,81 Muts/MB	positive  TC 10%, IC<1%	3,81	MSS
<u>322</u>	69	Female	KRAS:c.35G>T (p.Gly12Val)  SMAD4:c.1066C>A (p.Pro356Thr)  TGFBR2:c.1115T>C (p.Leu372Pro)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0,79%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):3,8 Muts/MB	negative  TC<1%, IC<1%	3,8	MSS
<u>323</u>	52	Male	Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):0,95 Muts/MB	negative  TC<1%, IC<1%	0,95	MSS

<u>324</u>	49	Female	IDH1:c.395G>T (p.Arg132Leu) MAP2K1:c.158 T>G (p.Phe53Cys) EPHA2:c.594C> G (p.Tyr198Ter) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 24,18% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,8 Muts/MB	negative  TC<1%, IC<1%	3,8	MSS
<u>325</u>	70	Male	KRAS:c.35G>A (p.Gly12Asp) MUTYH:c.734G> A (p.Arg245His) TP53:c.925_94 1del (p.Pro309LeufsTer22) Micros atellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 32,61% PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):0,95 Muts/MB	negative  TC<1%, IC<1%	0,95	MSS
<u>326</u>	71	Female	KRAS:c.34G>C (p.Gly12Arg) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):3.83 Muts/MB	negative  TC <1% IC<1%	3,83	MSS

<u>327</u>	72	Male	KRAS:c.35G>T (p.Gly12Val)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0%  PD-L1 expression:positive TC<1% IC 2%  Tumor Mutational Burden (TMB):0 Muts/MB	positive  T C<1% IC 2%	0	MSS
<u>328</u>	48	Female	RAD51:c.817C>T (p.Gln273Ter)  KRAS:c.35G>A (p.Gly12Asp)  TP53:c.824_833 del (p.Cys275LeufsTer67)  Micros atellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 11,06%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):6,64 Muts/MB	negative  TC<1%, IC<1%	6,64	MSS
<u>329</u>	67	Female	KRAS:c.35G>A (p.Gly12Asp)  RECQL4:c.3236+ 1G>C (splicing)  U2AF1:c.101C>T (p.Ser34Phe)  TP53:c.374C>T (p.Thr125Met)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):5.68 Muts/MB	negative  TC<1% IC<1%	5,68	MSS

<u>330</u>	66	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.818G>T (p.Arg273Leu) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):1.9 Muts/MB	negative  TC<1% IC<1%	1,9	MSS
<u>331</u>	74	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.423_424 delCCinsG (p.Cys141TrpfsTer29) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 1.24 % PD-L1 expression:positive TC 1% IC<1% Tumor Mutational Burden (TMB):2.85 Muts/MB	positive  TC 1% IC<1%	2,85	MSS
<u>332</u>	47	Female	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):3.78 Muts/MB	negative  TC <1% IC<1%	3,78	MSS
<u>333</u>	53	Female	KRAS:c.35G>T (p.Gly12Val) MPL:amplification TP63:amplification AR:amplification Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 5.74 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):4.76 Muts/MB	negative  TC <1% IC<1%	4,76	MSS

<u>334</u>	51	Male	KRAS:c.35G>T (p.Gly12Val) SMAD4:c.1081C>T (p.Arg361Cys) FAT1:c.4587_4588insCT (p.Thr1531SerfsTer12) PARP2:amplification Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 20.65 % PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):7.57 Muts/MB	negative  TC<1% IC<1%	7,57	MSS
<u>335</u>	70	Male	KRAS:c.35G>A (p.Gly12Asp) ARID1A:c.5573_5576delACTT (p.His1858ProfsTer24) TP53:c.707A>G (p.Tyr236Cys) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 9.06 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):2.84 Muts/MB	negative  TC <1% IC<1%	2,84	MSS
<u>336</u>	53	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.42delG (p.Ser15ValfsTer29) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 6.69 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):4.73 Muts/MB	negative  TC <1% IC<1%	4,73	MSS

<u>337</u>	65	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.428T>C (p.Val143Ala) TGFB2:c.1558 C>T (p.Arg520Ter) RASA2:c.1359+ 2T>C (splicing) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 11.11 % PD-L1 expression:-  Tumor Mutational Burden (TMB):4.73 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:HETEROZ YGOUS (6/7) DPD:WT	-	4,73	MSS
<u>338</u>	68	Male	NRAS:c.182A>G (p.Gln61Arg) BAP1:c.287_288 delTG (p.Leu96SerfsTer29) TP53:c.4 9delG (p.Glu17LysfsTer27) Microsat ellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 2.57 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):3.79 Muts/MB	negative  TC <1% IC<1%	3,79	MSS

<u>339</u>	71	Male	KRAS:c.34G>C (p.Gly12Arg)  ASXL1:c.427C>T (p.Arg143Ter)  KRAS:amplification  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 27,82%  PD-L1 expression:positive TC 30%, IC 15%  Tumor Mutational Burden (TMB):7,59 Muts/MB	positive  TC 30%, IC 15%	7,59	MSS
<u>340</u>	51	Female	KRAS:c.35G>T (p.Gly12Val)  RB1:c.1547G>A (p.Trp516Ter)			
<u>341</u>	73	Male	KRAS:c.35G>A (p.Gly12Asp)  CDKN2A:c.151-2A>G (splicing)  TGFBR2:c.190_191insA (p.Thr64AsnfsTer2)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0 %  PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):0.95 Muts/MB	negative  TC<1% IC<1%	0,95	MSS
<u>342</u>	65	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 33,06%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):3,79 Muts/MB  ERCC1:High expression  TYMS:Low expression	negative  TC<1%, IC<1%	3,79	MSS

<u>343</u>	63	Female	KRAS:c.34G>C (p.Gly12Arg)  Microsatellite Instability (MSI):-  Genomic Instability Score (GIS):GISL 3  Tumor Mutational Burden (TMB):1,89 Muts/MB		1,89	-
<u>344</u>	59	Female	MRE11A:c.1252_1253insA (p.Ile418AsnfsTer39)  KRAS:c. 34G>C (p.Gly12Arg)  DPYD:c.1905+1 G>A  TP53:c.192delC (p.Arg65GlufsTer58)  Microsat ellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 23,95%  PD-L1 expression:positive TC<1%, IC 1%  Tumor Mutational Burden (TMB):0,95 Muts/MB  ERCC1:High expression  TYMS:Low expression  UGT1A1:HOMOZY GOUS MUTATED (7/7)  DPD:HETEROZYGOUS	positive  T C<1%, IC 1%	0,95	MSS
<u>345</u>	53	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):8,55 Muts/MB	negative  TC<1%, IC<1%	8,55	MSS

<u>346</u>	58	Male	KRAS:c.38G>A (p.Gly13Asp) PMS1:c.793C>T (p.Arg265Ter) TP53:c.488A>G (p.Tyr163Cys)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHL 0 %  PD-L1 expression:positive TC <1% IC 15% Tumor Mutational Burden (TMB):9.51 Muts/MB	positive  T C <1% IC 15%	9,51	MSS
<u>347</u>	51	Male	FANCL:c.2T>C (p.Met1?) FGFR2 fusion:FGFR2(17) - CCDC6(2)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 38,17%  PD-L1 expression:negative TC<1%, IC<1%  Tumor Mutational Burden (TMB):2,84 Muts/MB	negative  TC<1%, IC<1%	2,84	MSS
<u>348</u>	66	Female	KRAS:c.34G>T (p.Gly12Cys)  SMAD4:c.1309- 3A>G ( )  RNF43:c.153_154insATCA (p.Pro521IlefsTer24)  RNASEH2 B:c.3G>A (p.Met1?)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 16.61 %  PD-L1 expression:negative TC <1% IC<1%  Tumor Mutational Burden (TMB):6.65 Muts/MB	negative  TC <1% IC<1%	6,65	MSS

<u>349</u>	71	Female	KRAS:c.35G>T (p.Gly12Val) DPYD:c.1905+1G>A BLM:c.1882+1G>A KMT2C:c.11460+1delG (splicing) TP53:c.473_473delGinsTT (p.Arg158LeufsTer23) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 10.74 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):2.86 Muts/MB	negative TC <1% IC<1%	2,86	MSS
<u>350</u>	66	Male	KRAS:c.34G>C (p.Gly12Arg)			
<u>351</u>	55	Female	KRAS:c.35G>A (p.Gly12Asp) SMAD4:c.1096C>T (p.Gln366Ter) TP53:c.1013del (p.Phe338SerfsTer7) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 10.02 % PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2.84 Muts/MB ERCC1:Low expression TYMS:Low expression	negative TC<1% IC<1%	2,84	MSS

<u>352</u>	61	Male	PALB2:c.719delC (p.Pro240LeufsTer39) KRAS:c. 35G>T (p.Gly12Val) SMAD4:c.533C> G (p.Ser178Ter) PARP1:c.2848+ 3A>G ( ) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 33.95 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):7.59 Muts/MB ERCC1:High expression TYMS:Low expression	negative  TC <1% IC<1%	7,59	MSS
<u>353</u>	48	Male	PTEN:c.760A>T (p.Lys254Ter) APC:c.4435del G (p.Val1479SerfsTer28) Micros atellite Instability (MSI):MSS PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):FAIL Muts/MB	negative  TC <1% IC<1%	FAIL	MSS
<u>354</u>	68	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.777_778 insC (p.Ser260LeufsTer4) Microsat ellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):3.8 Muts/MB	negative  TC <1% IC<1%	3,8	MSS

<u>355</u>	62	Male	BRCA2:BRCA2 gene duplication KRAS:c.35G>A (p.Gly12Asp) SMAD4:c.1336C>T (p.Gln446Ter) JAK2:amplification Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 31% PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):5.7 Muts/MB	negative  TC<1% IC<1%	5,7	MSS
<u>356</u>	63	Female	KRAS:c.34G>T (p.Gly12Cys) DPYD:c.1905+1G>A STK11:c.527A>T (p.Asp176Val) STK11:c.527A>T (p.Asp176Val) TP53:c.853G>A (p.Glu285Lys) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 0% PD-L1 expression:positive TC 1% IC<1% Tumor Mutational Burden (TMB):9.49 Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:HETEROZYGOUS (6/7) DPD:HETEROZYGOUS	positive  TC 1% IC<1%	9,49	MSS
<u>357</u>	83	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.499C>T (p.Gln167Ter)			

<u>358</u>	47	Female	KRAS:c.35G>T (p.Gly12Val) CHEK2:c.470T>C (p.Ile157Thr) CDKN2A:c.291_292delGC (p.His98ProfsTer21) TP53:c.844C>T (p.Arg282Trp) TP53:c.578A>T (p.His193Leu) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):8.65 Muts/MB	negative  TC<1% IC<1%	8,65	MSS
<u>359</u>	68	Male	BRCA2: BRAF:c.1462_1476del ACAGCACCTACACCT (p.Thr488_Pro492del) TP53:c.659A>G (p.Tyr220Cys) CCNE1:amplification Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 34.81 % PD-L1 expression:negative TC <1% IC<1% Tumor Mutational Burden (TMB):0.95 Muts/MB	negative  TC <1% IC<1%	0,95	MSS

<u>360</u>	54	Female	KRAS:c.35G>A (p.Gly12Asp)  SMAD4:c.1333C>T (p.Arg445Ter)  TP53:c.725G>A (p.Cys242Tyr)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC 5%, IC<1%  Tumor Mutational Burden (TMB):1,9 Muts/MB  ERCC1:Low expression  TYMS:Low expression	positive  TC 5%, IC<1%	1,9	MSS
<u>361</u>	71	Male	KRAS:c.35G>A (p.Gly12Asp)  FANCL:c.1110_1113dup (p.Thr372AsnfsTer13)  CDKN2A:c.181G>T (p.Glu61Ter)  SMARCA4:c.2741delT (p.Leu914ArgfsTer36)  TP53:c.527G>A (p.Cys176Tyr)  Microsatellite Instability (MSI):MSS  Loss of Heterozygosity (LOH):LOHH 16,2%  PD-L1 expression:positive TC 1%, IC<1%  Tumor Mutational Burden (TMB):6,64 Muts/MB  ERCC1:Low expression  TYMS:Low expression	positive  TC 1%, IC<1%	6,64	MSS

<u>362</u>	75	Female	KRAS:c.35G>T (p.Gly12Val) TP53:c.817C>T (p.Arg273Cys) SMAD4:c.1333 C>T (p.Arg445Ter) RB1:c.219_220 dup (p.Ala74GlufsTer4) Microsatel lite Instability (MSI):MSS PD- L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):1,9 Muts/MB	negative  TC<1%, IC<1%	1,9	MSS
<u>363</u>	39	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.586C>T (p.Arg196Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):0 Muts/MB	negative  TC<1%, IC<1%	0	MSS
<u>364</u>	51	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.673- 1G>A (splicing) KMT2C:c.3869delG (p.Arg1290LysfsTer13) Micros atellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):1,9 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1%, IC<1%	1,9	MSS

<u>365</u>	81	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.524G>A (p.Arg175His)  Microsatellite Instability (MSI):MSS  PD-L1 expression:positive TC<1% IC 5% Tumor Mutational Burden (TMB):1.9 Muts/MB	positive  TC<1% IC 5%	1,9	MSS
<u>366</u>	41	Female	KRAS:c.182_184delinsGAA (p.Gln61_Glu62delinsArgLys)  TP53:c.319_320dup (p.Gly108ThrfsTer16)  Microsatellite Instability (MSI):MSS Tumor Mutational Burden (TMB):1.9 Muts/MB		1,9	MSS
<u>367</u>	58	Male	KRAS:c.35G>A (p.Gly12Asp)  Microsatellite Instability (MSI):MSS  PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):6,67 Muts/MB	negative  TC<1%, IC<1%	6,67	MSS
<u>368</u>	41	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.817C>T (p.Arg273Cys) ARID1A:c.3664_3668delGGGCGinsAGC (p.Gly1222SerfsTer5)  Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):2,84 Muts/MB	negative  TC<1%, IC<1%	2,84	MSS

<u>369</u>	48	Male	KRAS:c.34G>C (p.Gly12Arg) TP53:c.916C>T (p.Arg306Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):1.91 Muts/MB	negative  TC<1% IC<1%	1,91	MSS
<u>370</u>	71	Female	KRAS:c.35G>A (p.Gly12Asp) TP53:c.725G>T (p.Cys242Phe) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,76 Muts/MB	negative  TC<1%, IC<1%	4,76	MSS
<u>371</u>	71	Female	KRAS:c.34G>C (p.Gly12Arg) SMAD4:c.1052A >T (p.Asp351Val) RNF43:c.433C> T (p.Arg145Ter) TP53:c.637C>T (p.Arg213Ter) AURKA:c.1187 _1188del (p.Lys396ArgfsTer4) Microsat ellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):6.65 Muts/MB	negative  TC<1% IC<1%	6,65	MSS

<u>372</u>	74	Male	KRAS:c.35G>T (p.Gly12Val) CDKN2A:c.153_154insG (p.Met52AspfsTer68) ARID1A:c.5202T>A (p.Tyr1734Ter) TP53:c.743G>A (p.Arg248Gln) RASA1:c.1288C>T (p.Gln430Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1% IC 10% Tumor Mutational Burden (TMB):7.62 Muts/MB	positive TC<1% IC 10%	7,62	MSS
<u>373</u>	58	Female	Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB): Muts/MB	negative TC<1%, IC<1%		MSS
<u>374</u>	67	Male	KRAS:c.34G>C (p.Gly12Arg) CDKN2A:c.45G>A (p.Trp15Ter) KDM6A:c.2588_2589insA (p.Ser864GlufsTer11) TP53:c.713G>A (p.Cys238Tyr) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):2.85 Muts/MB	negative TC<1% IC<1%	2,85	MSS

<u>375</u>	60	Male	KRAS:c.35G>T (p.Gly12Val) PIK3CA:c.3139C>T (p.His1047Tyr) MAP2K7:c.289C>T (p.Gln97Ter) TP53:c.734G>A (p.Gly245Asp) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHL 12.67 % PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2.85 Muts/MB	negative TC<1% IC<1%	2,85	MSS
<u>376</u>	59	Male	KRAS:c.35G>T (p.Gly12Val) CDKN2A:c.174_207del (p.Val59ProfsTer76) TP53:c.723delC (p.Cys242AlafsTer5) CCND2:amplification Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):2.87 Muts/MB ERCC1:Low expression TYMS:Low expression UGT1A1:HETEROZYGOUS (6/7) DPD:WT	negative TC<1% IC<1%	2,87	MSS

<u>377</u>	37	Female	KRAS:c.35G>T (p.Gly12Val) SMAD4:c.431C>A (p.Ser144Ter) TP53:c.469G>C (p.Val157Leu) RNF43:c.1624_1651del (p.Gln543AlafsTer148) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):4,76 Muts/MB	negative TC<1%, IC<1%	4,76	MSS
<u>378</u>	61	Male	KRAS:c.38G>A (p.Gly13Asp) BAP1:c.783+2T>C CDKN2A:c.151-1G>T (splicing) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1%, IC 2% Tumor Mutational Burden (TMB):5,71 Muts/MB	positive TC<1%, IC 2%	5,71	MSS
<u>379</u>	45	Male	KRAS:c.182_183delinsTG (p.Gln61Leu) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):1.93 Muts/MB	negative TC<1% IC<1%	1,93	MSS

<u>380</u>	55	Male	BRCA1:gene duplication KRAS:c.35G>A (p.Gly12Asp) CDKN2A:c.329G>A (p.Trp110Ter) TP53:c.637C>T (p.Arg213Ter) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 24.82 % PD-L1 expression:negative TC<1% IC<1% Tumor Mutational Burden (TMB):3.82 Muts/MB	negative  TC<1% IC<1%	3,82	MSS
<u>381</u>	36	Male	KRAS:c.35G>T (p.Gly12Val) SMAD4:c.170_173del (p.Leu57Ter) TP53:c.646G>T (p.Val216Leu) Microsatellite Instability (MSI):MSS Tumor Mutational Burden (TMB):1,9 Muts/MB		1,9	MSS
<u>382</u>	49	Male	PALB2:c.2257C>T (p.Arg753Ter) KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,8 Muts/MB	negative  TC<1%, IC<1%	3,8	MSS
<u>383</u>	66	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.820G>T (p.Val274Phe) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1%, IC<1% Tumor Mutational Burden (TMB):4,75 Muts/MB	positive  TC<1%, IC<1%	4,75	MSS

<u>384</u>	59	Female	WT1:c.662-1G>T (splicing) TP53:c.673-2A>G (splicing) Microsatellite Instability (MSI):MSS Loss of Heterozygosity (LOH):LOHH 61.85 % PD-L1 expression:positive TC1% IC<1% Tumor Mutational Burden (TMB):5.71 Muts/MB	positive TC1% IC<1%	5,71	MSS
<u>385</u>	63	Female	KRAS:c.35G>A (p.Gly12Asp) Microsatellite Instability (MSI):MSS Tumor Mutational Burden (TMB):7.64 Muts/MB		7,64	MSS
<u>386</u>	84	Female	KRAS:c.34G>C (p.Gly12Arg) TP53:c.376-2A>G (splicing) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,8 Muts/MB	negative TC<1%, IC<1%	3,8	MSS
<u>387</u>	80	Male	KRAS:c.34G>C (p.Gly12Arg)			
<u>388</u>	86	Female	KRAS:c.35G>T (p.Gly12Val) PIK3CA:c.1636C>G (p.Gln546Glu) ARID2:c.1750G>T (p.Glu584Ter) TP53:c.844C>T (p.Arg282Trp) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1%, IC<1% Tumor Mutational Burden (TMB):3,82 Muts/MB	negative TC<1%, IC<1%	3,82	MSS

<u>389</u>	59	Male	KRAS:c.35G>T (p.Gly12Val) ARID1A:c.6105_6106dup (p.Glu2036GlyfsTer7) SMAD4:c.1037delC (p.Pro346LeufsTer38) TP53:c.596G>T (p.Gly199Val) Microsatellite Instability (MSI):MSS Tumor Mutational Burden (TMB):3.8 Muts/MB		3,8	MSS
<u>390</u>	73	Male	KRAS:c.35G>A (p.Gly12Asp) CDKN2A:c.130deIT (p.Tyr44ThrfsTer9) TP53:c.711G>T (p.Met237Ile) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC 30% IC<1% Tumor Mutational Burden (TMB):FAIL Muts/MB	positive TC 30% IC<1%	FAIL	MSS
<u>391</u>	48	Male	FANCL:c.2T>C (p.Ala2_Met74del) KRAS:c.35G>A (p.Gly12Asp) TP53:c.660T>G (p.Tyr220Ter) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):7.6 Muts/MB	negative TC<1% IC<1%	7,6	MSS

<u>392</u>	62	Male	ATM:c.9170G>C (p.Ter3057Ser) GNAS:c.601C>T (p.Arg201Cys) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):3.9 Muts/MB ERCC1:Low expression TYMS:Low expression	negative  TC<1% IC<1%	3,9	MSS
<u>393</u>	82	Male	KRAS:c.35G>A (p.Gly12Asp) AKT1:c.49G>A (p.Glu17Lys) CTNNB1:c.97T>G (p.Ser33Ala) Microsatellite Instability (MSI):MSS PD-L1 expression:negative TC<1% IC<1%  Tumor Mutational Burden (TMB):12.34 Muts/MB	negative  TC<1% IC<1%	12,34	MSS
<u>394</u>	65	Male	Microsatellite Instability (MSI):MSS Tumor Mutational Burden (TMB):1.92 Muts/MB ERCC1:High expression TYMS:Low expression UGT1A1:WT (6/6) DPD:WT		1,92	MSS

<u>395</u>	79	Female	KRAS:c.182A>G (p.Gln61Arg) TP53:c.586C>T (p.Arg196Ter) RNF43:c.1111C>T (p.Arg371Ter) PPP2R1A:c.548G>A (p.Arg183Gln) FGFR3 fusion:FGFR3(17) - TACC3(14) Microsatellite Instability (MSI):MSS PD-L1 expression:positive TC<1%, IC 5% Tumor Mutational Burden (TMB):6,63 Muts/MB	positive TC<1%, IC 5%	6,63	MSS
<u>396</u>	61	Female	KRAS c.35G>A p.Gly12Asp SF3B1 c.2098A>G p.Lys700Glu TP53 c.451C>T p.Pro151Ser1	positive TC10% IC<1%	0	MSS
<u>397</u>	69	Male	KRAS:c.34G>C (p.Gly12Arg) KRAS:c.183A>C (p.Gln61His) PTEN:c.987_990 delTAAA (p.Asn329LysfsTer14) PTEN:c.955_958delACTT (p.Thr319Ter) TP53:c.380C>T (p.Ser127Phe) TP53:c.701A>G (p.Tyr234Cys)	negative TC<1% IC<1%	16,38	MSS
<u>398</u>	65	Female	KRAS:c.35G>A (p.Gly12Asp) ERBB2:amplification	negative TC<1%, IC<1%	0	MSS
<u>399</u>	77	Female	KRAS:c.35G>A (p.Gly12Asp) ARID2:c.1189C>T (p.Gln397Ter) TP53:c.683_686del (p.Asp228ValfsTer18)	negative TC<1% IC<1%	4,78	MSS

<u>400</u>	65	Male	KRAS:c.35G>A (p.Gly12Asp) TP53:c.743G>A (p.Arg248Gln)	negative  TC<1% IC<1%	5,72	MSS
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